

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana
Millennium Pharmaceuticals, Inc.

<120> 14171 Protein Kinase, A Novel Human
Protein Kinase and Uses Thereof

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<151> 2001-02-12

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Ser Gly Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser Ala			
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Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Pro Ser			
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Cys His Arg Val Arg Asp Thr Ser Lys Leu Met Lys Ile Leu Gln Pro			
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Gln Asp Val Asp Leu Ala Leu Asp Ser Gly Ala Ser Leu Leu His Leu			
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Asn Ala Asn Pro Asn Leu Ser Asn Arg Arg Gly Ser Thr Pro Leu His			
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act gtc aag ctg ctt gtc gag gag aag gcc gat gtg ctg gcc cgg gga	2116
Thr Val Lys Leu Leu Val Glu Glu Lys Ala Asp Val Leu Ala Arg Gly	
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ccc ctg aac cag acg cgc ctg cac ctg gct gcc gcc cac ggg cac tgg	2164
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ggccaccttc	ccatctgcaa	gctctgtggc	aagacgcggg	gggtgaagtg	gaacgccag	1800
acgcttgatg	ggagagacgc	attgcactct	ccgcacagc	gcgggcacta	ccgcgtgtgc	1860
cgatcctcca	tcgacctgtg	ctccgacgtc	aacgtctgca	cctgtctggc	acagagacc	1920
ctgcacatgg	ccgcggagac	ggggcacacg	agcactgcca	tggtctcttc	gcacgtgggc	1980
ctgtggcaag	aggcgctgac	ctcagacgac	tacacgcgtc	gctacctggc	tgcgccgaac	2040
ggacacttgc	ccaactgtcaa	gctgcttgtc	gaggagaagc	ccgatgtact	ggcccgggga	2100
ccaccttgag	agacggcgct	gcactctgtc	gcgcgccaac	ggagctcgga	gttggttgag	2160
gagttgtcca	gcgcgcgatg	catgttagct	ctgcagagc	aggggtcag	ctggctgcac	2220
ctggccgcct	agggccggca	cgcacagacg	ttagagactc	tgtgcctcag	cgvgggccac	2280
atacaactgc	agagctccaa	gttccagggc	ggccatggcc	ccgcgccac	ctctatgcg	2340
cgaacacga	ctcag					2355

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<210> 4
<211> 272
<212> PRT
<213> Artificial Sequence
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<220>

<223> Consensus Protein Kinase Domain

<400> 4

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Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
 1          5          10
Lys Ala Lys His Lys Thr Gly Lys Ile Val Ala Val Lys Ile Leu Lys
 20          25          30
Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys Arg Leu Ser
 35          40          45
His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp Thr Asp Asp
 50          55          60
His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Asp Leu Phe Asp
 65          70          75
Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala Lys Lys Ile
 85          90          95
Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Asn Gly Ile
100          105          110
Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Asn Gly
115          120          125
Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Leu Glu Lys Leu
130          135          140
Thr Thr Phe Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile
145          150          155
Leu Glu Gly Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly
165          170          175
Val Ile Leu Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala
180          185          190
Asp Leu Pro Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile
195          200          205
Phe Val Leu Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile
210          215          220
Asp Pro Leu Glu Glu Leu Phe Arg Ile Lys Lys Arg Arg Leu Pro Leu
225          230          235
Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Cys Leu
245          250          255
Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
260          265          270
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<210> 5

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence for ATP binding

<220>

<221> VARIANT

<222> 1

<223> The Xaa at position 1 can be Leu, Ile or Val.

<220>

<221> VARIANT

<222> 3, 5

<223> The Xaa at positions 3 and 5 can be any amino acid residue except Pro.

<220>

<221> VARIANT
 <222> 6
 <223> The Xaa at position 6 can be Phe, Tyr, Trp, Met,
 Gly, Ser, Thr, Asn, or His.

<220>
 <221> VARIANT
 <222> 7
 <223> The Xaa at position 7 can be Ser, Gly or Ala.

<220>
 <221> VARIANT
 <222> 8
 <223> The Xaa at position 8 can be any amino acid except
 Pro or Trp.

<220>
 <221> VARIANT
 <222> 9
 <223> The Xaa at position 9 can be Leu, Ile, Val, Cys,
 Ala or Thr.

<220>
 <221> VARIANT
 <222> 10
 <223> The Xaa at position 10 can be any amino acid
 except Pro or Asp.

<220>
 <221> VARIANT
 <222> 11
 <223> The Xaa at position 11 can be any amino acid.

<220>
 <221> VARIANT
 <222> 12
 <223> The Xaa at position 12 can be Gly, Ser, Thr, Ala,
 Cys, Leu, Ile, Val, Met, Phe or Tyr.

<220>
 <221> VARIANT
 <222> (13)...(30)
 <223> The Xaa at positions 13 to 30 can be any amino
 acid.

<220>
 <221> VARIANT
 <222> (13)...(30)
 <223> The number of Xaa residues in this portion of the
 consensus can vary between 5 residues and 18
 residues.

<220>
 <221> VARIANT
 <222> 31
 <223> The Xaa at position 31 can be Leu, Ile, Val, Met,
 Phe, Tyr, Trp, Cys, Ser, Thr, Ala, or Arg.

<220>
 <221> VARIANT
 <222> 32

<223> The Xaa at position 32 can be Ala, Ile, Val or Pro.

<220>
 <221> VARIANT
 <222> 33
 <223> The Xaa at position 33 can be Leu, Ile, Val, Met, Phe, Ala, Gly, Cys, Lys, or Arg.

<400> 5
 Xaa Gly Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Lys

<210> 6
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence for serine/threonine kinase active site

<220>
 <221> VARIANT
 <222> 1
 <223> The Xaa at position 1 can be Leu, Ile, Val, Met, Phe, Tyr or Cys.

<220>
 <221> VARIANT
 <222> 2,4,8,9
 <223> The Xaa at positions 2, 4, 8 or 9 can be any amino acid residue.

<220>
 <221> VARIANT
 <222> 3
 <223> The amino acid residue at position 3 can be His or Tyr.

<220>
 <221> VARIANT
 <222> 6
 <223> The amino acid residue at position 6 can be Leu, Ile, Val, Met, Phe or Tyr.

<220>
 <221> VARIANT
 <222> 11,12,13
 <223> The Xaa at positions 11, 12, or 13 can be Leu, Ile, Val, Met, Phe, Tyr, Cys or Thr.

<400> 6
 Xaa Xaa Xaa Xaa Asp Xaa Lys Xaa Xaa Asn Xaa Xaa Xaa
 1 5 10

<210> 7
 <211> 12
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> consensus sequence for aspartyl protease active site

 <220>
 <221> VARIANT
 <222> 1
 <223> The Xaa at position 1 can be Leu, Ile, Val, Met,
 Phe, Gly, Ala or Cys.

 <220>
 <221> VARIANT
 <222> 2
 <223> The Xaa at position 2 can be Leu, Ile, Val, Met,
 Thr, Ala, Asp or Asn.

 <220>
 <221> VARIANT
 <222> 3
 <223> The Xaa at position 3 can be Leu, Ile, Val, Phe,
 Ser or Ala.

 <220>
 <221> VARIANT
 <222> 5
 <223> The Xaa at position 5 can be Ser or Thr.

 <220>
 <221> VARIANT
 <222> 7
 <223> The Xaa at position 7 can be Ser, Thr, Ala or Val.

 <220>
 <221> VARIANT
 <222> 8
 <223> The Xaa at position 8 can be Ser, Thr, Ala, Pro,
 Asp, Glu, Asn, or Gln.

 <220>
 <221> VARIANT
 <222> 9, 11
 <223> The Xaa at positions 9 and 11 can be any amino
 acid residue.

 <220>
 <221> VARIANT
 <222> 10
 <223> The Xaa at position 10 can be Leu, Ile, Val, Met,
 Phe, Ser Thr, Asn, or Cys.

 <220>
 <221> VARIANT
 <222> 12
 <223> The Xaa at position 12 can be Leu, Ile, Val, Met,
 Phe, Gly, Thr or Ala.

 <400> 7

Xaa Xaa Xaa Asp Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10

<210> 8
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence for ankyrin domain

<400> 8
 Asp Gly Arg Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Glu
 1 5 10 15
 Val Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Val Asn Ala Arg Asp
 20 25 30
 Lys

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> forward primer

<400> 9
 ggcacggaag atcagtggtca 20

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> reverse primer

<400> 10
 cgaggcggttc ttctccaaca 20

<210> 11
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> probe

<400> 11
 agggctgttc actggtctc atcctt 26

<210> 12
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>

<223> primer

<400> 12 36
gatgtggttg aattcatgga gggcgacggc gggacc

<210> 13
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13 39
gatgctggct ctagaggtct tgcttcgccg caggagtgt

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 14 21
tccgagttgc tgtcacagtt g

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 15 19
cgatgggagc ttgcattca

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> probe

<400> 16 23
tcccagactc ttgaaggccc cga

<210> 17
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 17
Gln Ser Leu Lys Phe Gln Gly Gly His Gly Pro Ala Ala Thr Leu Leu
1 5 10 15
Arg Arg Ser Lys Thr

<210> 18
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic peptide

<400> 18
 Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Ser Lys Leu Pro Ser
 1 5 10 15
 Ser Gly Ser Gly
 20

<210> 19
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic peptide

<400> 19
 Ser Glu Thr Glu Asp Leu Cys Glu Lys Pro Asp Asp Glu Val Lys Glu
 1 5 10 15
 Thr Ala His Asp
 20

<210> 20
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic peptide

<221> SITE
 <222> 1
 <223> A biotin is covalently attached to the residue at
 position 1.

<400> 20
 Lys Lys Arg Phe Ser Phe Lys Lys Ser Phe Lys Leu Ser Gly Phe Ser
 1 5 10 15
 Phe Lys

<210> 21
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> siRNA target sequence

<400> 21
 aagaacatcc tgcacatcat g 21

 <210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> siRNA target sequence

 <400> 22
 aagaagatgg agatggccaa g 21

 <210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> siRNA target sequence

 <400> 23
 aaccttcaac cagcgatctg g 21

 <210> 24
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> siRNA sense strand, nucleotides 1-21 are
 ribonucleic acid, nucleotides 22 and 23 are
 deoxyribonucleic acid.

 <400> 24
 aagaacaucc ugcacaucau gtt 23

 <210> 25
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> siRNA anti-sense strand, complement of SEQ ID
 NO:24, nucleotides 1-21 are ribonucleic acid,
 nucleotides 22-23 are deoxyribonucleic acid.

 <400> 25
 caugaugugc aggauguucu utt 23

 <210> 26
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> siRNA sense strand, nucleotides 1-21 are
 ribonucleic acid, nucleotides 22 and 23 are
 deoxyribonucleic acid.

<400> 26
 aagaagaugg agauggccaa gtt 23

<210> 27
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> siRNA anti-sense strand, complement of SEQ ID
 NO:26, nucleotides 1-21 are ribonucleic acid,
 nucleotides 22 and 23 are deoxyribonucleic acid.

<400> 27
 cuuggccauc uccaucuuc utt 23

<210> 28
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> siRNA sense strand, nucleotides 1-21 are
 ribonucleic acid, nucleotides 22 and 23 are
 deoxyribonucleic acid.

<400> 28
 aaccuuaac cagcgauucg gtt 23

<210> 29
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> siRNA anti-sense strand, complement of SEQ ID
 NO:28, nucleotides 1-21 are ribonucleic acid,
 nucleotides 22 and 23 are deoxyribonucleic acid.

<400> 29
 ccagaucgcu gguugaaggu utt 23